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DATE: Wednesday, January 18, 2006

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☐	L4	myb	3135
☐	L5	L4 and stress	1233
☐	L6	L5 and (transgenic or transform?)	931
☐	L7	L6 and plant	818
☐	L8	L7 and (abiotic or biotic)	129
☐	L9	L8 and (cold or salt or dehydration)	127
☐	L10	L9 and y11414	1
☐	L11	l4 and y11414	1

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NEWS 10	JAN 13	New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to INPADOC
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=> file agricola caplus biosis

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=> s myb
L1 6242 MYB

=> s l1 stress
MISSING OPERATOR L1 STRESS
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l1 and stress
L2 219 L1 AND STRESS

=> s l2 and (transgenic or transform?)
L3 78 L2 AND (TRANSGENIC OR TRANSFORM?)

=> s l3 and Y11414
L4 1 L3 AND Y11414

=> dup rem l3
PROCESSING COMPLETED FOR L3
L5 59 DUP REM L3 (19 DUPLICATES REMOVED)

=> d l5 1-59 ti

L5 ANSWER 1 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Methods for regulating **stress** tolerance in **transgenic** plants by transcription factor HOS9, or by cold **stress**-related genes from HOS9 regulon identified by expression profiling

L5 ANSWER 2 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Gene expression profiling in molecular toxicology modeling using robust multi-array averaging and partial least squares algorithms

L5 ANSWER 3 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI SNOW1 protein interacting with ICE1 and regulating expression of the CBF3 gene in response to freezing **stress** in Arabidopsis

L5 ANSWER 4 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Nucleic acids encoding transcription factors from Eucalyptus grandis and Pinus radiata and their use for plant **transformation**

L5 ANSWER 5 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI The curcuminoids- and anthocyanins-responsive genes in human adipocytes and their use in screenings of anti-obesity and anti-diabetes drugs

L5 ANSWER 6 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Novel pathway for megakaryocyte production after in vivo conditional eradication of integrin αIIb-expressing cells

L5 ANSWER 7 OF 59 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN DUPLICATE 1
TI Cloning and characterization of a drought-inducible **MYB** gene from Boea crassifolia.

L5 ANSWER 8 OF 59 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

TI Structural and functional role of the human ARC/Mediator coactivator in specific gene regulatory pathways.

L5 ANSWER 9 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 2
TI Sequences of human schizophrenia related genes and use for diagnosis, prognosis and therapy

L5 ANSWER 10 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Systems, methods and kits for characterizing phosphoproteomes by digestion, chromatography and mass spectrometry

L5 ANSWER 11 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Cell proliferation-related polypeptides and encoding nucleic acids in rice and their uses for plant **transformation**

L5 ANSWER 12 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI **Transgenic** maize with enhanced phenotype

L5 ANSWER 13 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Use of specific **myb** gene Y11414 for the production of **transgenic** plants tolerant to biotic and abiotic **stresses**

L5 ANSWER 14 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Expression of inflammatory and septic genes to identify antiinflammatory and antiseptic peptides for therapeutic use

L5 ANSWER 15 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Protein and cDNA sequences of plant **Myb** domain-containing transcription factors and uses for crop improvement

L5 ANSWER 16 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Concerted effect of **transforming** growth factor-β, cyclin inhibitor p21, and c-myc on smooth muscle cell proliferation

L5 ANSWER 17 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI ABA activates ADPR cyclase and cADPR induces a subset of ABA-responsive genes in Arabidopsis

L5 ANSWER 18 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI **MYB** transcription factors are differentially expressed and regulated during secondary vascular tissue development in hybrid Aspen

L5 ANSWER 19 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI **Stress**-related transcription factors of rice and their cDNA sequences

L5 ANSWER 20 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Heat-stable, protease-resistant chaperonin-like oligomeric proteins of plants, cDNAs encoding them and their use in the expression of foreign genes in plants

L5 ANSWER 21 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3
TI Salt tolerance-related protein STO binds to a **Myb** transcription factor homologue and confers salt tolerance in Arabidopsis

L5 ANSWER 22 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Expression of anthocyanins and proanthocyanidins after **transformation** of alfalfa with maize Lc

L5 ANSWER 23 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Cloning and characterization of cDNAs associated with the embryogenic dedifferentiation of tobacco immature pollen grains

L5 ANSWER 24 OF 59 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on

STN
TI Molecular profile of the anti-myeloma activity of histone deacetylase (HDAC) inhibitors: Biological and therapeutic implications.

L5 ANSWER 25 OF 59 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN DUPLICATE 4
TI Arabidopsis AtMYC2 (bHLH) and AtMYB2 (**MYB**) function as transcriptional activators in abscisic acid signaling.

L5 ANSWER 26 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Isolation of two genes similar to DREB1/CBF from the sweet cherry and their analysis by **transformation** into Arabidopsis

L5 ANSWER 27 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Heat-stable, protease-resistant chaperonin-like oligomeric proteins of plants, cDNAs encoding them and their use in the expression of foreign genes in plants

L5 ANSWER 28 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI cDNA sequence of Arabidopsis PAP1 and PAP2 gene and its uses of regulation of anthocyanin pigment synthesis in **transgenic** plants

L5 ANSWER 29 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Endocrine disruptor screening using DNA chips of endocrine disruptor-responsive genes

L5 ANSWER 30 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI The vascular expression pattern directed by the Eucalyptus gunnii cinnamyl alcohol dehydrogenase EgCAD2 promoter is conserved among woody and herbaceous plant species

L5 ANSWER 31 OF 59 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Identification of Dysregulated Genes in Myeloma Using a Genetically Identical Twin Samples.

L5 ANSWER 32 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Transcription factor **stress**-related proteins and methods of use in plants

L5 ANSWER 33 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI cDNA sequences of polynucleotides from peppermint oil gland and their uses

L5 ANSWER 34 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Endogenous gene expression assay

L5 ANSWER 35 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI The roles of plant **MYB** transcription factors in abiotic **stresses**, phenypropanoid metabolic pathway and anthocyanin pathway

L5 ANSWER 36 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Cloning of a vascular-specific promoter from rice Oshox1 gene and its use in making **transgenic** plants

L5 ANSWER 37 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI A conserved **MYB** transcription factor involved in phosphate starvation signaling both in vascular plants and in unicellular algae

L5 ANSWER 38 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Gene expression profiling of amyloid beta peptide-stimulated human post-mortem brain microglia

L5 ANSWER 39 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Identification of novel molecules and pathogenic pathways in primary biliary cirrhosis: cDNA array analysis of intrahepatic differential gene expression

L5 ANSWER 40 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI A novel jasmonic acid-inducible rice **myb** gene associates with fungal infection and host cell death

L5 ANSWER 41 OF 59 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI The Ets family contains transcriptional activators and repressors involved in angiogenesis.

L5 ANSWER 42 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI The TATA box and a **Myb** binding site are essential for anaerobic expression of a maize GapC4 minimal promoter in tobacco

L5 ANSWER 43 OF 59 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI rd22BP1(MYC) and ATMYB2(**MYB**) act as transcriptional activators in ABA signaling.

L5 ANSWER 44 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI **Transgenic** plants expressing genes for enzymes of methionine biosynthesis showing improved tolerance of **stress** conditions

L5 ANSWER 45 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 5
TI **MYB**-related transcription factor NtMYB2 induced by wounding and elicitors is a regulator of the tobacco retrotransposon Tto1 and defense-related genes

L5 ANSWER 46 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Arabidopsis DNA encoding a Mg2+, Zn2+/H+ exchanger, and **transgenic** plants with enhanced **stress** tolerance

L5 ANSWER 47 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI A prolonged cold treatment-induced cytochrome P450 gene from Arabidopsis thaliana

L5 ANSWER 48 OF 59 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN DUPLICATE 6
TI Altered patterns of gene expression in Arabidopsis elicited by cauliflower mosaic virus (CaMV) infection and by a CaMV gene VI transgene.

L5 ANSWER 49 OF 59 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN DUPLICATE 7
TI Ectopic expression of a novel **MYB** gene modifies the architecture of the Arabidopsis inflorescence.

L5 ANSWER 50 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Expression cloning in Fe2+ transport defective yeast of a novel maize MYC transcription factor

L5 ANSWER 51 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Molecular pathology of liver fibrosis

L5 ANSWER 52 OF 59 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved.

(2006) on STN DUPLICATE 8
TI Role of Arabidopsis MYC and **MYB** homologs in drought- and abscisic acid-regulated gene expression.

L5 ANSWER 53 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Oncogene- and tumor-suppressor gene-related proteins in plants and fungi

L5 ANSWER 54 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 9
TI Activation of hepatic stellate cells by TGFα and collagen type I is mediated by oxidative **stress** through c-**myb** expression

L5 ANSWER 55 OF 59 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved.
(2006) on STN DUPLICATE 10
TI Two classes of cis sequences contribute to tissue-specific expression of a PAL2 promoter in **transgenic** tobacco.

L5 ANSWER 56 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Identification of a cis-regulatory region of a gene in Arabidopsis thaliana whose induction by dehydration is mediated by abscisic acid and requires protein synthesis

L5 ANSWER 57 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 11
TI Regulation of genes that are induced by drought **stress** in Arabidopsis thaliana

L5 ANSWER 58 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI The carboxy-terminal domain of c-**Myb** activates reporter gene expression in yeast

L5 ANSWER 59 OF 59 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved.
(2006) on STN DUPLICATE 12
TI An Arabidopsis **myb** homolog is induced by dehydration **stress** and its gene product binds to the conserved **MYB** recognition sequence.

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(FILE 'HOME' ENTERED AT 19:12:03 ON 18 JAN 2006)

FILE 'AGRICOLA, CAPLUS, BIOSIS' ENTERED AT 19:12:54 ON 18 JAN 2006
L1 6242 S MYB
L2 219 S L1 AND STRESS
L3 78 S L2 AND (TRANSGENIC OR TRANSFORM?)
L4 1 S L3 AND Y11414
L5 59 DUP REM L3 (19 DUPLICATES REMOVED)

=> d l4

L4 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:80884 CAPLUS
DN 140:123683
TI Use of specific **myb** gene **Y11414** for the production of **transgenic** plants tolerant to biotic and abiotic **stresses**
IN Coraggio, Immacolata; Locatelli, Franca; Bracale, Marcella; Vannini, Candida
PA Consiglio Nazionale Delle Ricerche, Italy; Universita' Degli Studi Dell'insubria
SO PCT Int. Appl., 15 pp.
CODEN: PIXXD2

DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2004009822	A2	20040129	WO 2003-IB2878	20030721
	WO 2004009822	A3	20040722		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	CA 2492919	AA	20040129	CA 2003-2492919	20030721
	EP 1525316	A2	20050427	EP 2003-765231	20030721
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
	JP 2005533498	T2	20051110	JP 2004-522602	20030721
	US 2005204431	A1	20050915	US 2005-521811	20050419
PRAI	IT 2002-MI1624	A	20020723		
	WO 2003-IB2878	W	20030721		

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FILE 'AGRICOLA, CAPLUS, BIOSIS' ENTERED AT 19:12:54 ON 18 JAN 2006
L1 6242 S MYB
L2 219 S L1 AND STRESS
L3 78 S L2 AND (TRANSGENIC OR TRANSFORM?)
L4 1 S L3 AND Y11414
L5 59 DUP REM L3 (19 DUPLICATES REMOVED)

=> d l5 1-59 ab

L5 ANSWER 1 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The invention provides methods and compns. to confer or improve or increase **stress** tolerance in particular freezing or cold tolerance in plants. These methods include overexpressing HOS9 protein or its homolog to modulate (up-regulate or down-regulate) one or more downstream target genes. The inventors found, that an Arabidopsis homeodomain transcription factor HOS9 mediates cold tolerance through a pathway independent from C repeat (CRT)/dehydration responsive element (DRE) binding factor (CBF). An Arabidopsis mutant hos9-1 (high expression of osmotically responsive genes) displays several altered phenotypic features, including increased sensitivity to freezing **stress**. Thus, HOS9 is homeobox transcription factor that controls **stress** tolerance in plants by modulating the activity of a number of cold-responsive genes. The inventors identified HOS9-regulated genes using microarray gene expression profiling. The invention provides **transgenic** plant, cell, seed and expression vectors that include a nucleic acid sequence derived from HOS9 or from genes from HOS9 regulon that confer or improve cold tolerance.

L5 ANSWER 2 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The present invention is based on methods of predicting toxicity of test agents and methods of generating toxicity prediction models using algorithms for analyzing quant. gene expression information. The invention also includes computer systems comprising the toxicity

prediction models, as well as methods of using the computer systems by remote users for determining the toxicity of test agents.

L5 ANSWER 3 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The SNOW1 protein playing a role in the transcriptional response to cold **stress** in Arabidopsis thaliana is identified and the gene encoding it is cloned. SNOW1 interacts with ICE1 to activate transcription of the CBF3 gene. CBF3 directs transcription of genes associated with the response to cold **stress**. SNOW1 was identified as a ubiquitous and constitutive protein localized in the nucleus. Expression of the SNOW1 gene is higher in plants homozygous for a mutant allele of the ICE1 gene. Two-hybrid assays showed that SNOW1 and ICE1 had a specific interaction and SNOW1 interacts with the **MYB**-binding site of the CBF3 gene to induce transcription.

L5 ANSWER 4 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The invention provides a large number of cDNA sequences encoding proteins containing transcription factor motifs from Eucalyptus grandis and Pinus radiata. Microarray oligonucleotide probes for the polynucleotides are also provided. The nucleic acids may be used to **transform** plants to regulate gene expression involved in lignin quality and structure, wood composition, plant fiber composition, plant cell division, and plant development.

L5 ANSWER 5 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The curcuminoids- and anthocyanins-responsive gene expression profiles in adipocytes have been revealed. The curcuminoids- and anthocyanins-responsive genes are designed to be used as the index markers in the screenings of the substances that can affect the gene expression patterns in obesity and diabetes. These substances can be the candidates of anti-obesity and anti-diabetes drugs. Therefore, the groups of curcuminoids- and anthocyanins-responsive genes are intended to be used as markers in a form of kit such as DNA chip for the screening of anti-obesity and anti-diabetes drugs.

L5 ANSWER 6 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB Our knowledge of the mol. mechanisms that regulate hematopoiesis in physiol. and pathol. conditions is limited. Using a mol. approach based on cDNA microarrays, we demonstrated the emergence of an alternative pathway for mature bone marrow cell recovery after the programmed and reversible eradication of CD41+ cells in **transgenic** mice expressing a conditional toxigene targeted by the platelet αIIb promoter. The expression profile of the newly produced CD41+ cells showed high levels of transcripts encoding Ezh2, TdT, Rag2, and various Ig heavy chains. In this context, we identified and characterized a novel population of Lin-Sca-1hic-Kit- cells, with a lymphoid-like expression pattern, potentially involved in the reconstitution process. Our study revealed novel transcriptional cross talk between myeloid and lymphoid lineages and identified gene expression modifications that occur in vivo under these particular **stress** conditions, opening important prospects for therapeutic applications.

L5 ANSWER 7 OF 59 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN DUPLICATE 1

L5 ANSWER 8 OF 59 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
AB The mammalian Activator Recruited Cofactor (ARC)/Mediator family of transcriptional co-activator complexes is directly targeted by many gene activators to assist with recruitment of RNA polymerase 11 to target genes. We are identifying subunits of this similar to 2 MDa complex that directly interact with transcriptional activators to elucidate the role of

the ARC/Mediator in specific gene regulatory pathways. We now report that the human ARC105/MED15 subunit is a functionally important target of the activation domains of several transactivators, including the TGF-beta-regulated SMAD2/3, the cholesterol-regulated SREBP, and the **stress**-response factor NF-kB/p65. Structural studies with NMR demonstrate that the ARC105/MED15 subunit harbors an activator-targeted domain related to the KIX domain found in the CBP/p300 family of co-activators. Intriguingly, the ARC105/MED15 KIX domain mediates interaction with the activation domains of SREBP and NF-kB/p65, but not with the activation domains of the CBP/p300 KIX binding activators CREB and c-**Myb**, indicating that different KIX domainsplay unique roles in gene regulation. The activator-targeted yeast Mediator subunit Gal I I also harbors a functional KIX domain, suggesting that ARC105/MED15 and Gal11 are homologous subunits. We have now identified the pleiotropic drug resistance protein 1 (PDR1) transcription factor as a Gal I I KIX domain interaction partner. Our genetic studies have confirmed the critical and specific importance of Gal11 in PDR1 function and in multiple drug resistance in yeast.

L5 ANSWER 9 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 2
AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing and monitoring diseases using gene-specific and/or tissue-specific primers. The present invention also describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen. [This abstract record is one of 3 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L5 ANSWER 10 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The invention provides systems, software, methods and kits for detecting and/or quantifying phosphorylatable polypeptides and/or acetylated polypeptides in complex mixts., such as a lysate of a cell or cellular compartment (e.g., such as an organelle). The methods can be used in high throughput assays to profile phosphoproteomes and to correlate sites and amts. of phosphorylation with particular cell states.

L5 ANSWER 11 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB Disclosed are proteins, and nucleic acids encoding such proteins, involved in or associated with cell proliferation, senesence, differentiation, development, and **stress** response in rice (Oryza sativa). The proteins are identified in yeast two-hybrid assays, in which they bind to a bait fragment of rice E2F1, 018989-4003, E2F2, S49462, CYCOS2, MADS45, RAP1B, MADS6, FDRMADS8, MADS3, MADS5, MADS15, HOS59, GF14-c, DAD1, 006819-2510, CRTC, SGT1, ERP, CHIB1, CS, PP2A-2, or CAA90866. Thus, the invention provides networks of proteins interacting with rice MADS box transcription factors, proteins containing homeobox domains, protein that interact at the thylakoid of chloroplast, proteins associated with senescence., protein that interact with the cell wall in response to biotic **stress**, and proteins interacting with serine/threonine protein phosphatases. Also disclosed are production of the proteins in recombinant system, and uses for such proteins in **transgenic** plants.

L5 ANSWER 12 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The current invention provides **transgenic** maize with an enhanced phenotype from insertion of heterologous DNA. Enhanced phenotypes include yield such as yield under **stress** conditions, quality of plant morphol., physiol. or seed composition, metabolic function, cell growth, and the like. Such **transgenic** maize is produced by generating a plurality of **transgenic** events for a plurality of unique

transgenic DNA constructs where each of the **transgenic** events comprises introducing into the genome of a parental maize line a single **transgenic** DNA construct comprising a promoter operably linked to heterologous DNA in sufficient quantity to produce **transgenic** cells which can be cultured into plants of **transgenic** maize having the enhanced phenotype. Examples of transgenes include nucleic acids encoding TOC1-like receiver domain 3, HY5-like protein, proline permease, RR3-like receiver domain 8, ARR2-like receiver domain, **myb** transcription vector, SVP-like protein, a cytochrome P 450, and HSF protein. The construction of a plasmid vector, pMON72472, for Agrobacterium-mediated **transformation** of maize callus cells is provided. The present invention claimed a total of 736 sequences, but the Sequence Listing was not made available on publication of the patent application.

L5 ANSWER 13 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The present invention relates to the use of **myb** class R2R3 gene Y11414 or its functional homologs for the production of plants tolerant to biotic **stresses**, salt-induced, dehydration-induced, oxidative, osmotic **stresses**. The gene Y11414 is under control of CaMV35S promoter and upstream of the terminator of gene Nos. The binary expression cassettes carrying gene Y11414 was introduced by electroporation into GV3101 strain of Agrobacterium tumefaciens, which was then used for **transforming** Arabidopsis thaliana plants with the "floral dip" methods.

L5 ANSWER 14 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB A method of identifying a polynucleotide or pattern of polynucleotides regulated by one or more sepsis or inflammatory inducing agents and inhibited by a peptide is described. A method of identifying a pattern of polynucleotide expression for inhibition of an inflammatory or septic response. The method includes contacting human epithelial cells with LPS, LTA, CpG DNA and/or intact microbe or microbial components in the presence or absence of a cationic peptide; detecting a pattern of polynucleotide expression for the cells in the presence and absence of the peptide, wherein the pattern in the presence of the peptide represents inhibition of an inflammatory or septic response. Also included are compds. and agents identified by the methods of the invention. In another aspect, the invention provides methods and compds. for enhancing innate immunity in a subject.

L5 ANSWER 15 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB Disclosed herein are inventions in the field of plant biochem. and genetics. The invention provides the protein and cDNA sequences of plant **Myb** transcription factors encoded by gene G225, G226 and G682. **Transgenic** plants and seeds with improved biol. characteristics can be obtained by use of said **Myb** transcription factors. The invention relates to improving the yield of **transgenic** crops grown in a nutrient (phosphorus) deficient environment or nitrogen deficient environment by expressing in roots a **Myb** domain-containing transcription factors. The invention relates to production of **transgenic** crops with increased seed oil or having improved drought tolerance.

L5 ANSWER 16 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB Increased aortic smooth muscle cell (SMC) proliferation is a key event in the pathogenesis of atherosclerosis. **Transforming** growth factor-β (TGF-β) is one of the potent inhibitors of SMC proliferation. The purpose of this study was to explore the effect of TGF-β inhibition on proliferation of SMC and expression of growth regulatory mols. like p21 and c-myc, and to determine whether restoration of cell cycle regulatory mols. normalizes the altered proliferation. To test the role of TGF-β in SMC proliferation, using antisense plasmid DNA, the authors inhibited TGF-β gene from aortic SMC, which resulted in a

significant increase ($P < 0.03$) in proliferation (studied by quantifying new DNA synthesis with [3H]thymidine uptake assay). In TGF-β-altered SMC (TASMC), the mRNA expression (studied by RT-PCR) of c-myc was increased, whereas that of the cyclin inhibitor p21 was completely inhibited. Using p21 sense plasmid DNA, the authors transfected p21 gene in TASMC, which restored p21 mRNA and protein expression and decreased proliferation ($P < 0.002$) in TASMC. Similar treatment with c-myc antisense oligonucleotides significantly ($P < 0.001$) decreased the proliferation of TASMC. TASMC also exhibited alteration in morphol. changes in SMC but returned to normal with treatment of p21 and TGF-β sense plasmid DNA. Two-dimensional gel electrophoresis anal. of SMC and TASMC demonstrated differential expression of proteins relevant to cellular proliferation and atherosclerosis. This study uniquely analyzes the effect of TGF-β at the mol. level on proliferation of SMC and on cell cycle regulatory mols., implicating their potential role in the pathogenesis of atherosclerosis.

L5 ANSWER 17 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB Cyclic ADP-ribose (cADPR) was previously shown to activate transient expression of two abscisic acid (ABA)-responsive genes in tomato cells. Here, the authors show that the activity of the enzyme responsible for cADPR synthesis, ADP-ribosyl (ADPR) cyclase, is rapidly induced by ABA in both wild-type (WT) and abi1-1 mutant Arabidopsis plants in the absence of protein synthesis. Furthermore, in **transgenic** Arabidopsis plants, induced expression of the Aplysia ADPR cyclase gene resulted in an increase in ADPR cyclase activity and cADPR levels, as well as elevated expression of ABA-responsive genes KIN2, RD22, RD29a, and COR47 (although to a lesser extent than after ABA induction). Genome-wide profiling indicated that about 28% of all ABA-responsive genes in Arabidopsis are similarly up- and downregulated by cADPR and contributed to the identification of new ABA-responsive genes. These results suggest that activation of ADPR cyclase is an early ABA-signaling event partially insensitive to the abi1-1 mutation and that an increase in cADPR plays an important role in downstream mol. and physiol. ABA responses.

L5 ANSWER 18 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB More than 120,000 poplar ESTs have been sequenced from 20 different cDNA libraries by the Swedish Center for Tree Functional Genomics. Authors screened this EST collection for **MYB** transcription factors involved in secondary vascular tissue formation, and genes assigned as PttMYB3Ra, PttMYB4a and PttMYB21a were selected for further characterization. Three **MYB** genes showed different expression patterns in various organs, tissues and stem sub-sections representing different developmental stages of vascular tissue formation. Furthermore, the anal. showed that PttMYB21a expression was much higher in secondary cell wall formation zone of xylem and phloem fibers than in other developmental zones. **Transgenic** hybrid aspen plants, expressing the 3'-part of the PttMYB21a gene in antisense orientation were generated to assess the function of PttMYB21a gene in vascular tissue formation and lignification. All **transgenic** lines showed reduced growth and had fewer internodes compared to the wild-type. The anal. of selected lines showed that acid soluble lignin present in the bark was higher in **transgenic** lines as compared to wild-type plants. Moreover a higher transcript level of caffeoyl-CoA 3-O-methyltransferase [CCoAOMT]; EC 2.1.1.104 was found in the phloem of the **transgenic** plants, suggesting that PttMYB21a might function as a transcriptional repressor.

L5 ANSWER 19 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB Seventy polynucleotides encoding transcription factors of cereals and in particular rice are provided. The transcription factors of can be classified into known families, including zinc finger proteins, **Myb** transcription factors, WRKY transcription factors, IAA7 transcription factors, AP2/EREBP-type transcription factors, leucine zipper transcription factors, bZIP transcription factors, and homeo-domain

transcription factors. Potential **stress**-related genes which encode known or putative transcription factors on the Arabidopsis GeneChip (Affymetrix) were identified based on the annotation associated with probe sets on the chip and by searching for conserved domains for AP2/EREBPs. **Myb** proteins, bZIPs, and WRKY zinc finger proteins. Rice orthologs of the Arabidopsis transcription factors genes are identified by reverse genetics and by blasting the full-length cDNA sequences of 402 Arabidopsis transcription factor genes against an internal rice database composed of about 45,000 predicted full-length rice genes. Expression profiling of the rice transcription factors is achieved using a proprietary rice GeneChip Rice Genome Array (Affymetrix). Also provided are recombinant vectors, expression cassettes, host cells and plants containing the polynucleotides. Methods for using the polynucleotides to alter resistance or tolerance of plants to **stress**, alter biol. pathways, and alter gene expression are also provided.

L5 ANSWER 20 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB Proteins that are resistant to chemical and heat denaturation, that oligomerize and that have chaperonin-like activities are purified from a number of plants and characterized. Genes for the proteins, known as stable proteins or SPs are cloned and characterized. These proteins may be useful in the stabilization, refolding, repairing, preventing aggregation and de-aggregation of macromols. such as proteins in vivo and in vitro. The proteins were identified as a boiling-stable and acetone insol. Fraction of exts. of a number of plants. The SP1 protein from aspen was a monomer of 12.4 kilodaltons that formed an oligomer of 116 kilodaltons. The oligomer was stable when boiled with SDS at ratios of SDS:SP1 of 600:1 and was also essentially stable to proteinase K at 37° for 60 min. The oligomer stabilized a heat-labile citrate synthase against thermal denaturation at ratios of synthase:SP1 oligomer of 1:50 or greater. A cDNA was cloned by antibody screening of an expression library in a λ expression vector. The antibody to the protein was used to determine levels of cross-reacting materials in tomato leaf. The levels of cross-reacting material were increased when the leaves had been subjected to salt or drought **stress**.

L5 ANSWER 21 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3
AB Regulating the intracellular Na+/K+ ratio is an essential process for salinity tolerance. The yeast mutant, can, which is deficient in calcineurin, can not grow on medium containing Na+ because it is unable to regulate the intracellular Na+/K+ ratio. Expression of the STO gene of Arabidopsis thaliana in the can mutant complements the salt-sensitive phenotype. A protein of Arabidopsis, an H-protein promoter binding factor (HPPBF-1), that binds to STO protein was isolated. HPPBF-1 cDNA has a sequence encoding a **Myb** DNA binding-motif and its gene expression is induced by salt **stress**. Furthermore, HPPBF-1 protein is localized in the nucleus. Although, the expression level of STO is not induced under salt-**stress** conditions, overexpression of STO in a **transgenic** Arabidopsis plant gave it a higher salt tolerance than was observed in the wild type. When STO **transgenic** plants and wild-type plants were subjected to salt **stress**, root growth was increased by 33-70% in the **transgenic** plants under salt **stress**. These results suggest that STO is involved in salt-**stress** responses in Arabidopsis.

L5 ANSWER 22 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB Three anthocyanin regulatory genes of maize (Zea mays; Lc, B-Peru, and C1) were introduced into alfalfa (Medicago sativa) in a strategy designed to stimulate the flavonoid pathway and alter the composition of flavonoids produced in forage. Lc constructs included a full-length gene and a gene with a shortened 5'-untranslated region. Lc RNA was strongly expressed in Lc **transgenic** alfalfa foliage, but accumulation of red-purple anthocyanin was observed only under conditions of high light intensity or low temperature These **stress** conditions induced chalcone synthase and

flavanone 3-hydroxylase expression in Lc **transgenic** alfalfa foliage compared with non-**transformed** plants. Genotypes containing the Lc transgene construct with a full-length 5'-untranslated region responded more quickly to **stress** conditions and with a more extreme phenotype. High-performance liquid chromatog. anal. of field-grown tissue indicated that flavone content was reduced in forage of the Lc **transgenic** plants. Leucocyanidin reductase, the enzyme that controls entry of metabolites into the proanthocyanidin pathway, was activated both in foliage and in developing seeds of the Lc **transgenic** alfalfa genotypes. Proanthocyanidin polymer was accumulated in the forage, but (+)-catechin monomers were not detected. B-Peru **transgenic** and C1 **transgenic** populations displayed no visible phenotypic changes, although these transgenes were expressed at detectable levels. These results support the emerging picture of Lc transgene-specific patterns of expression in different recipient species. These results demonstrate that proanthocyanidin biosynthesis can be stimulated in alfalfa forage using an myc-like transgene, and they pave the way for the development of high quality, bloat-safe cultivars with ruminal protein bypass.

L5 ANSWER 23 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN

AB We conducted differential screening to obtain cDNAs showing that gene expression is highly associated with the **transformation** from immature pollen to embryogenic cell, so-called embryogenic dedifferentiation of pollen, in a Nicotiana tabacum pollen culture system and analyzed their expression and sequences. Seventy-seven cDNA clones were independently isolated and distinguished into 16 groups based on their sequences. The groups were further categorized into two classes, Class I and II, based on the gene expression pattern of the representative clone of each group under various pollen culture conditions arranged for examining the coincidence with the dedifferentiation. The 13 groups in Class I showed prominent expression under the conditions allowing or facilitating pollen dedifferentiation and the expression level increased earlier than A-type cyclin genes, but they were not markedly expressed in the cell populations rich in S-phase cells, i.e. young anthers with pollen mother cells, BY-2 cells at the growth phase and early phase embryos derived from immature pollen. The other three groups in Class II encoded homologs to H1 histone, H2A histone and minichromosome maintenance (MCM) protein, resp. The level of their transcripts increased during dedifferentiation, but it was also high in anthers containing pollen mother cells and in the proliferating BY-2 cells indicating that their expression is coincident with the S phase but not with dedifferentiation. These findings suggest that pollen dedifferentiation is a complex process accompanied with the reentrance of cell cycle and unknown events probably caused by specific expression of many genes, at least, listed in Class I. These genes should be used as reliable markers and important clues for further studies on the mol. mechanism of dedifferentiation.

L5 ANSWER 24 OF 59 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

AB Histone deacetylases (HDACs) affect cell differentiation and survival at the transcriptional level, by regulating the acetylation status of nucleosomal histones and the function of transcription factor complexes. HDAC inhibition induces differentiation and/or apoptosis in **transformed** cells. We recently showed (Blood 2003;101:4055) that the prototypic hydroxamic acid-based HDAC inhibitor suberoylanilide hydroxamic acid (SAHA), potently induces cell death of human multiple myeloma (MM) cells (even those resistant to conventional or novel anti-tumor agents); sensitizes MM cells to Fas or TRAIL receptor-mediated apoptosis; and inhibits IL-6 secretion in co-cultures of bone marrow stromal cells (BMSCs) with MM cells. These pleiotropic effects of SAHA on MM cells directly and on their microenvironment prompted us to further investigate the molecular sequelae of SAHA, with particular focus on the transcriptional profile of SAHA-treatment, since HDAC inhibition exerts

its anti-tumor activity predominantly by targeting the regulation of gene expression. Although HDAC inhibition was originally pursued to induce differentiation of malignant cells, by de-repressing transcriptional programs of cellular differentiation, our gene expression profiling (with U133A Affymetrix microarrays) and subsequent confirmatory mechanistic/functional assays, indicate that HDAC inhibition in MM triggers a distinct transcriptional signature characterized by suppression of pathways critical for tumor cell proliferation, survival and drug resistance. Specifically SAHA downregulates insulin-like growth factor (IGF)/IGF-1 receptor and IL-6R signaling cascades; anti-apoptotic molecules (e.g. caspase inhibitors); oncogenes (e.g. **myb**, maf, Axl, polo and Aurora kinases, abl, vav); DNA synthesis or repair enzymes; transcription factors (e.g. XBP-1, E2F-1); nucleocytoplasmic transport regulators; and adhesion molecules (e.g. RHAMM, intergrins) implicated in MM pathophysiology. SAHA treatment upregulates p53 and represses HIF-1alpha and NF-kappaB activity, suppresses 26S proteasome subunits and proteasome activity, but does not trigger major heat shock protein upregulation, in contrast to pronounced **stress** responses generated by MM cell treatment with other drugs, e.g. proteasome inhibitors. SAHA enhances MM cell sensitivity to other anti-MM agents, including dexamethasone, cytotoxic chemotherapy, thalidomide analogs, proteasome inhibitors or hsp90 inhibitors. SAHA treatment does not indiscriminately suppress or activate gene transcription: it modulates expression of specific functional gene clusters with direct or indirect involvement in tumorigenesis, proliferation, survival and drug-resistance of MM cells, specifically, or malignant cells, in general. This indicates that HDAC function is critical for MM cells by actively maintaining a transcriptional program indispensable for their uncontrolled proliferation and/or inappropriate resistance to pro-apoptotic stimuli. The pleiotropic anti-MM effects of SAHA, its ability to sensitize MM cells to multiple conventional or novel agents and, importantly, the fact that it had a favorable profile of side effects and achieved objective responses after oral administration in phase I clinical trials, provide the framework for future clinical trials of SAHA in MM.

L5 ANSWER 25 OF 59 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN DUPLICATE 4

AB In Arabidopsis, the induction of a dehydration-responsive gene, rd22, is mediated by abscisic acid (ABA). We reported previously that MYC and **MYB** recognition sites in the rd22 promoter region function as cis-acting elements in the drought- and ABA-induced gene expression of rd22. bHLH- and **MYB**-related transcription factors, rd22BP1 (renamed AtMYC2) and AtMYB2, interact specifically with the MYC and **MYB** recognition sites, respectively, in vitro and activate the transcription of the beta-glucuronidase reporter gene driven by the MYC and **MYB** recognition sites in Arabidopsis leaf protoplasts. Here, we show that **transgenic** plants overexpressing AtMYC2 and/or AtMYB2 cDNAs have higher sensitivity to ABA. The ABA-induced gene expression of rd22 and AtADH1 was enhanced in these **transgenic** plants. Microarray analysis of the **transgenic** plants overexpressing both AtMYC2 and AtMYB2 cDNAs revealed that several ABA-inducible genes also are upregulated in the **transgenic** plants. By contrast, a Ds insertion mutant of the AtMYC2 gene was less sensitive to ABA and showed significantly decreased ABA-induced gene expression of rd22 and AtADH1. These results indicate that both AtMYC2 and AtMYB2 proteins function as transcriptional activators in ABA-inducible gene expression under drought **stress** in plants.

L5 ANSWER 26 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN

AB DREB1 (dehydration responsive element binding protein 1)/CBF (C-repeat binding factor) up-regulates the expression of a group of genes designated as COR (cold regulated)/RD (responsive to dehydration) genes in

Arabidopsis at low temperature We isolated three DREB1/CBF-like genomic clones from the sweet cherry. Two (D2A and D2B) were deduced to be complete ORFs. Each putative protein had an EREBP/AP2 DNA binding domain motif, a potential nuclear localization signal, in the N-terminal. The conserved EREBP/AP2 domain of the D2 proteins showed high identity (74.apprx.79%) with each DREB1/CBF protein. In addition, TATA-box and G-box sequences, and **MYB**- and MYC-recognition sites were predicted in the 5'-region of each gene. Low temps. induced expression of the D2 genes in sweet cherry. Therefore, we renamed D2A and D2B as CIGA (cold induced gene A) and CIGB, resp. To investigate the effects of the CIG proteins at low temps., we **transformed** a binary vector carrying a fusion of the enhanced CaMV 35S promoter and CIGB into Arabidopsis using the floral dip method. Both neomycin phosphotransferase and the CIGB gene were detected in only five **transgenic** plants by PCR. Some **transgenic** plants had a dwarf phenotype. Although we are currently studying the expression of the CIG gene and its effects on freezing tolerance in the **transgenic** progeny, we postulate that this phenomenon is due to the transgene.

L5 ANSWER 27 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB Proteins that are resistant to chemical and heat denaturation, that oligomerize and that have chaperonin-like activities are purified from a number of plants and characterized. Genes for the proteins, known as stable proteins or SPs are cloned and characterized. These proteins may be useful in the stabilization, refolding, repairing, preventing aggregation and de-aggregation of macromols. such as proteins in vivo and in vitro. The proteins were identified as a boiling-stable and acetone insol. fraction of exts. of a number of plants. The SP1 protein from aspen was a monomer of 12.4 kilodaltons that formed an oligomer of 116 kilodaltons. The oligomer was stable when boiled with SDS at ratios of SDS:SP1 of 600:1 and was also essentially stable to proteinase K at 37° for 60 min. The oligomer stabilized a heat-labile citrate synthase against thermal denaturation at ratios of synthase:SP1 oligomer of 1:50 or greater. A cDNA was cloned by antibody screening of an expression library in a λ expression vector. The antibody to the protein was used to determine levels of cross-reacting materials in tomato leaf. The levels of cross-reacting material were increased when the leaves had been subjected to salt or drought **stress**.

L5 ANSWER 28 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB A method for determining gene expression in **transgenic** plants is disclosed. CDNA sequence of two genes, PAP1 and PAP2, cloned from Arabidopsis by activation tagging method were disclosed. The PAP1 and PAP2 and belong to R2, R3 **MYB** family and the genes were mapped to Arabidopsis chromosome 1 81 cm and 84 cm, resp. This method includes providing expression vectors having the PAP1 or PAP2 gene linked to an expressed gene of interest. If the expression vector is activated, the PAP1 or PAP2 genes confer a purple pigmentation to the **transgenic** plant. Thus, plants that have been successfully **transformed** are easily identifiable by visual inspection.

L5 ANSWER 29 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB A method and kit for detecting endocrine-disrupting chems. using DNA microarrays are claimed. The method comprises preparing a nucleic acid sample containing mRNAs or cDNAs originating in cells, tissues, or organisms which have been brought into contact with a sample containing the endocrine disruptor. The nucleic acid sample is hybridized with DNA microarrays having genes affected by the endocrine disruptor or DNA fragments originating in these genes have been fixed. The results obtained are then compared with the results obtained with the control sample to select the gene affected by the endocrine disruptor. Genes whose expression is altered by tri-Bu tin, 4-octaphenol, 4-nonylphenol, di-N-Bu phthalate, dichlorohexyl phthalate, octachlorostyrene, benzophenone, diethylhexyl phthalate, diethylstilbestrol (DES), and 17-β estradiol (E2), were found in mice by DNA chip anal.

L5 ANSWER 30 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN

AB Cinnamyl alc. dehydrogenase (CAD; EC 1.1.1.195) catalyzes the last step in the synthesis of the monomeric precursors of lignin. Here, we demonstrate that the vascular expression pattern conferred by the Eucalyptus gunnii EgCAD2 promoter in **transgenic** poplar (Populus tremula + Populus alba) is conserved in another perennial woody angiosperm of economic interest (Vitis vinifera L.), as well as in a model herbaceous plant (Nicotiana tabacum L.). Furthermore, promoter deletion anal. performed in both tobacco and poplar allowed us to identify the proximal region [-340/-124] as essential for vascular cambium/xylem-specific expression whereas the [-124/+117] region was shown to contain cis element-driving activity in phloem fibers. Interestingly, the [-340/-124] fragment contains an AC-rich cis-acting element present in numerous genes of the phenylpropanoid pathway expressed in xylem tissues, and known as a consensus **Myb** transcription factor binding site, suggesting that common **Myb** sites may provide a mechanism by which different steps of phenylpropanoid metabolism are coordinately regulated and expressed in vascular tissues. We have also shown in both tobacco and poplar that the EgCAD2 promoter is inducible by wounding and the cis-elements responsible for wounding responsiveness are located in the distal promoter region. Taken together, our data suggest that the mechanisms controlling developmental and wounding inducible expression of the EgCAD2 promoter are conserved among perennial woody and annual herbaceous plant species enabling us now to investigate in depth the transcriptional regulation of the EgCAD2 promoter in tobacco.

L5 ANSWER 31 OF 59 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

AB Genetic heterogeneity between individuals confounds the comparison of gene profiling of myeloma (MM) versus normal plasma cells. To overcome this barrier we compared expression profile of MM cells from a patient with plasma cells from a genetically identical twin. We purified CD138+ MM myeloma cells from the patient bone marrow and CD138+ plasma cells from the normal identical twin bone marrow. Total cellular RNA was prepared and subjected to cDNA microarrays with probe sets corresponding to more than 12,600 human genes (Affymetrix U95av2), followed by data analysis using DNA chip Analyzer (dchip). The results identify genes that are either induced or repressed in MM cells versus normal plasma cells. One hundred and three genes were upregulated in MM cells and 296 genes were downregulated with a lower bound of at least 3 fold change. Genes significantly increased in myeloma plasma cell included; those affecting the cell survival pathways (bcl-2 related proteins, dad-1, katanin p80, caspase 8 and FADD like apoptosis regulator); **stress** response genes (hsp90, hsp70, and hsp10); cell cycle related genes (CDC2-related kinase, CDK6, CDK7, Fzhr-1, p57/kip2, WIF-1); oncogenes/transcriptional factors (Jun-D, v-fos, **myb**, Xbp-1, RAN/ras, calmoduliun, Calnexin, NF-1, FGFR-3); and ubiquitin/proteasome pathway related genes (UbC, UbB, ubiquitin specific protease, proteasome sub unit alpha, Ubiquitin activating E1-like enzyme). Mitochondrial and ribosomal genes reflecting increased metabolic and translational activity were also increased in MM cells. The genes that were decreased in myeloma included development and differentiation-enhancing factor, protein inhibitor of STAT and apoptotic protease activating factor. These identified genes provide potential insight into mechanisms of malignant **transformation** in MM. For example, FGFR3 may lead to cell **transformation** and pathogenesis, xbp-1 to plasma cell differentiation, and bcl-2 related protein and dad-1 to anti apoptotic signals. Microarray results have been further confirmed by both northern and/or western blot analyses. These data may also have clinical implication. For example the high levels of Ubiquitin proteasome pathway related genes may confer increased sensitivity of MM to proteasome inhibitor therapy. The current study therefore identifies genes uniquely altered in MM cells versus normal plasma cells in an identical genotypic

background. These studies may help further understand MM etiology and pathogenesis and provide the framework to identify novel therapeutic targets.

L5 ANSWER 32 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The invention provides a method of producing a **transgenic** plant with a Transcription Factor **Stress**-Related Protein (TFSRP) coding nucleic acid, wherein expression of the nucleic acid sequence in the plant results in increased tolerance to environmental **stress** as compared to a wild type variety of the plant. Also provided are agricultural products, including seeds, produced by the **transgenic** plants. Also provided are isolated TFSRPs, and isolated nucleic acid coding TFSRPs, and vectors and host cells containing the latter.

L5 ANSWER 33 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB This invention provides 472 cDNA sequences of polynucleotides from peppermint which are expressed in plant oil gland cells, such as oil gland secretory cells of essential oil plants. The invention also provides the functional assignments for 151 of polypeptides derived from their cDNA sequences based on the sequence homologs. The polynucleotides provides in this invention can be used in as flavoring agent in food products and as scents in perfume.

L5 ANSWER 34 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The present invention relates to a method for evaluating the possible physiol. effects of a compound and/or a composition by assaying a cellular response through measurement of changes in expression levels of at least one endogenous gene. The present invention provides new means to identify environmental chems. or pharmaceutical compns. that interact with, amongst others, the endocrine system. The present invention thus relates to a method for detecting chems. that present a health threat. In one example of the invention, the effects of various estrogenic compds., on expression of pS2, MOA-A, TGFβ3, α1-ACT genes were investigated in MCF7 cells by DDRT-PCR. Furthermore, the scope of the present invention includes means to investigate the specific response of an individual to a certain treatment as well as a cellular state of disease through assaying the expression level(s) of one or more endogenous marker gene(s) in a sample taken from such an individual. The results of such investigations may be used in diagnosis and in therapy.

L5 ANSWER 35 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The present invention relates to nucleotides that encode **stress** tolerance-related **MYB** transcription factors, including MYB60, MYB74, MYB75 and MYB90. MYB74 gene was activated by **stress** both in an ABA dependent and an ABA independent pathway, while MYB60 gene was repressed by **stress** (particularly drought **stress**) in an ABA dependent manner. MYB75 and MYB90 genes were involved in regulating flavonoid biosynthesis, which is participant in the protection of plants against UV damage, oxidative **stress**, pathogen attack, etc. MYB75 and MYB90 genes activate the anthocyanin pathway. The invention further relates to uses of **MYB** transcription factors and to plants **transformed** by the nucleic acids. Addnl., the present invention relates to the production of **stress**-sensitive plants, which may be preferably used as environmental monitors.

L5 ANSWER 36 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The invention provides a vascular-specific promoter of HD-Zip (homeodomain leucine zipper) gene Oshox1 cloned from rice. The Oshox1 gene promoter can drive vascular-specific expression in rice and Arabidopsis, in all organs and at all developmental stages. The gene driven by this promoter has been shown to be involved in the formation of vascular tissue by inducing the cell fate commitment. Furthermore, the promoter according to the present invention has been shown to be active in guard cells, pollen and trichomes of the shoot and flower. Its expression can be induced upon

wounding. The Oshox1 gene promoter can be used to drive specific transgene expression in **transgenic** plants.

L5 ANSWER 37 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB Plants have evolved a number of adaptive responses to cope with growth in conditions of limited phosphate (Pi) supply involving biochem., metabolic, and developmental changes. We prepared an EMS-mutagenized M2 population of an Arabidopsis thaliana **transgenic** line harboring a reporter gene specifically responsive to Pi starvation (AtIPS1:: GUS), and screened for mutants altered in Pi starvation regulation. One of the mutants, phr1 (phosphate starvation response 1), displayed reduced response of AtIPS1::GUS to Pi starvation, and also showed impairment of a broad range of Pi starvation responses, including changes in responsiveness of various other Pi starvation-induced genes and metabolic responses, such as the increase in anthocyanin accumulation. PHR1 was positionally cloned and shown be related to the PHOSPHORUS STARVATION RESPONSE 1 (PSR1) gene from Chlamydomonas reinhardtii. A GFP::PHR1 protein fusion was localized in the nucleus independently of Pi status, as is the case for PSR1. PHR1 is expressed in Pi sufficient conditions and, in contrast to PSR1, is only weakly responsive to Pi starvation. PHR1, PSR1, and other members of the protein family share a **MYB** domain and a predicted coiled-coil (CC) domain, defining a subtype within the **MYB** superfamily, the **MYB**-CC family. Therefore, PHR1 was found to bind as a dimer to an imperfect palindromic sequence. PHR1-binding sequences are present in the promoter of Pi starvation-responsive structural genes, indicating that this protein acts downstream in the Pi starvation signaling pathway.

L5 ANSWER 38 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB Activation of microglia is a central part of the chronic inflammatory processes in Alzheimer's disease (AD). In the brains of AD patients, activated microglia are associated with amyloid beta (Aβ) peptide plaques. A number of previous studies have shown that aggregated synthetic Aβ peptide activates cultured microglia to produce a range inflammatory products. The full extent of the inflammatory response still remains to be determined In this study, gene array technol. was employed to investigate in a more extensive manner the consequences of microglial activation by Aβ peptide. RNA was prepared from pooled samples of cortical human microglia isolated from post-mortem cases and incubated with a low dose (2.5 μM) of Aβ1-42 (or peptide solvent) for 24 h. This material was used to prepare cDNA probes, which were used to detect the differential pattern of expressed genes on a 1,176 Clontech membrane gene array. Results obtained showed that 104 genes were either upregulated or downregulated by 1.67 fold or greater. The most highly induced genes belonged to the chemokine family with interleukin-8 (IL-8) expression being increased by 11.7 fold. Interestingly, many of the highly induced genes had been identified as being responsive to activation by the transcription factor NF-κB. A number of genes were downregulated. Thymosin beta, prothymosin alpha and parathymosin, all belonging to the same gene family, were downregulated. To validate these semi-quant. results, the expression of intercellular adhesion mol.-1 (ICAM-1) and rhoB were measured by RT-PCR in samples of cDNA derived from Aβ and control stimulated human cortical microglia. These results confirm the usefulness of the gene array approach for studying Aβ-mediated inflammatory processes.

L5 ANSWER 39 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB Primary biliary cirrhosis (PBC) is an autoimmune disease in which the pathogenesis of progressive liver injury is poorly understood. The aim was to provide novel insights into the pathogenesis of PBC related liver injury using cDNA array anal., which simultaneously examines expression of many genes. Utilizing cDNA arrays of 874 genes, PBC was compared with primary sclerosing cholangitis (PSC) associated cirrhosis and non-diseased liver. Differential expression of 10 genes was confirmed by real time quant. reverse transcriptase-polymerase chain reaction (RT-PCR). Array

anal. identified many differentially expressed genes that are important in inflammation, fibrosis, proliferation, signaling, apoptosis, and oxidative **stress**. PBC was associated with increased expression of both Th1 and Th2 type mols. of the immune response. Fibrosis related gene expression featured upregulation of connective tissue growth factor and **transforming** growth factor beta3. Many more apoptosis associated mols. exhibited increased expression, consistent with apoptosis being a more active and regulated process, in PSC associated cirrhosis than in PBC. Increased expression of many genes of the Wnt and notch pathways implicated these highly conserved and linked pathways in PBC pathogenesis. The observed increases in expression of c-jun, c-myc, and c-fos related antigen 1 are consistent with increased Wnt pathway activity in PBC. Differential expression of four components of the Wnt pathway, Wnt-5a, Wnt-13, FRITZ, and beta-catenin, was confirmed by quant. RT-PCR. Many genes implicated in intrahepatic inflammation, fibrosis, and regeneration were upregulated in PBC cirrhosis. In particular, increased expression of a number of Drosophila homologs was seen in PBC.

L5 ANSWER 40 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN

AB Endogenous signal mols. such as jasmonic acid (JA) and salicylic acid (SA) play an important role in induced resistance against pathogen infection and insect herbivore. In rice seedlings, JA is an effective inducer of systemic acquired resistance (SAR) against infection of blast fungus (Pyricularia grisea). To gain further insights into JA-mediated defense signaling pathways, we isolated and characterized a pathogen- and JA-induced rice gene (JAmyb) that encodes a **Myb** transcription factor. The JAmyb gene was induced within 1 day after fungal infection in resistant and susceptible interactions prior to lesion formation. Unlike most defense-related genes that are activated faster and stronger in resistant interactions, JAmyb induction by blast fungus is much higher in susceptible interactions, accompanied by large lesions and extensive tissue damage. Significant induction of JAmyb also was observed during cell death and lesion formation in certain lesion mimic mutants. Interestingly, JAmyb was activated rapidly by JA or wounding, independent of de novo protein synthesis, but not by other endogenous signal mols. such as SA and abscisic acid or SAR inducers such as benzothiadiazole and probenazole. We used SA-deficient **transgenic** plants to further demonstrate that depletion of SA in rice did not abolish but rather enhanced blast-induced JAmyb expression. These results suggest that JAmyb is related closely to host cell death and is involved in the JA-mediated, SA-independent signaling pathways in rice.

L5 ANSWER 41 OF 59 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

AB The Ets family contains a growing number of transcriptional activators and inhibitors, which activity is regulated by phosphorylation and protein-protein interactions. Among these factors, Ets1, Erg1 and Fli1 are expressed in endothelial cells during angiogenesis in normal and pathological development. The expression of these transcription factors is regulated by angiogenic factors in cultured endothelial cells, as well as by various **stresses** occurring during angiogenesis. Transfection experiments and **transgenic** mice analysis revealed that Ets family members are involved in the transcriptional regulation of endothelial specific genes such as those encoding Tie1 and -2, VEGFR1 and -2 and VE-Cadherin. In vitro studies plead for a role of Ets family members in endothelial cell adhesion, spreading and motility. Gene inactivation experiments show that Ets1 is dispensable for embryonic development. The phenotype of knocked-out embryos indicates that Te1 is required for maintenance of the developing vascular network in the yolk sac. Altogether, we suggest that Ets family members act both positively and negatively during the different steps of the angiogenic process. The regulation of the initiation of gene transcription arises from the combined activity of different transcriptional regulators. Therefore very few transcription factors are specific for a physiological process, or a

given cell type. The transcriptional network that regulates blood vessel formation involves transcription factors which are expressed in a variety of situations. The Lung Kruppel Like Factor (LKLF) which is required for blood vessel stabilisation during murine development is also expressed in the primitive vertebrae and in the lung of the adult (C.T. Kuo, M.L. Veselits, K.P. Barton, M.M. Lu, C. Clendenin, J.M. Leiden, The LKLF transcription factor is required for normal tunica media formation and blood vessel stabilisation during murine embryogenesis, Genes Dev. 11 (22) (1997) 2996-3006). Scl/Tal1 which is essential for angiogenic remodelling of the yolk sac capillary network (J.E. Visvader, Y. Fujiwara, S.H. Orkin, Unsuspected role for the T-cell leukemia protein SCL/tal-1 in vascular development, Genes Dev. 12 (4) (1998) 473-479), is involved in blood cell development and is also expressed in the developing brain. The EPAS transcription factor which was thought to be endothelial cell specific in the mouse embryo (H. Tian, S.L. McKnight, D.W. Russell, Endothelial PAS domain protein 1 (EPAS1), a transcription factor selectively expressed in endothelial cells, Genes Dev. 11 (1) (1997) 72-82) is also expressed in the liver, kidney and cells of the sympathetic nervous system of the chick embryo (J. Favier, H. Kempf, P. Corvol, J.M. Gasc, Cloning and expression pattern of EPAS1 in the chicken embryo. Colocalization with tyrosine hydroxylase, FEBS Lett. 462 (1-2) (1999) 19-24). Ets1, which expression was originally detected in lymphoid cells of adult tissues, has been the first transcription factor to be identified in endothelial cells during angiogenesis in the embryo (B. Vandenbunder, L. Pardanaud, T. Jaffredo, M.A. Mirabel, D. Stehelin, Complementary patterns of expression of c-ets1, c-**myb** and c-myc in the blood-forming system of the chick embryo, Development 107 (1989) 265-274) and in tumours (N. Wernert, M.B. Raes, P. Lassalle, M.P. Dehouck, B. Gosselin, B. Vandenbunder, D. Stehelin, The c-ets 1 proto-oncogene is a transcription factor expressed in endothelial cells during tumor vascularisation and other forms of angiogenesis in man, Am. J. Path. 140 (1992) 119-127). Since then, the Ets family has extended and this review will emphasise the relationships between these factors and angiogenesis.

L5 ANSWER 42 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN

AB The maize GapC4 promoter harbors a complex arrangement of cis-sequences involved in activation of anaerobic gene expression in tobacco. As shown by transient expression assays, four copies of a 50 bp anaerobic response element (ARE) increase anaerobic gene expression compared to the ARE alone. Expression strength is similar to a 190 bp fragment that contains most sequences required for anaerobic expression, including the 50 bp ARE. This supports the notion that redundancy of cis-acting sequences contribute to the anaerobic expression strength of the promoter. Mutation anal. of the 50 bp ARE revealed that cis-regulatory sequences are located within 30 bp at the 5' end of the ARE. Of these 30 bp a putative binding site for a **Myb** transcription factor is essential for anaerobic induction. The TATA box of the GapC4 promoter is also required for anaerobic gene expression and is bound specifically by a recombinant TATA box binding protein (TBP) from tobacco. A model for anaerobic induction of the GapC4 minimal promoter in tobacco that summarizes the presented data is discussed.

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L5 ANSWER 44 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN

AB The present invention provides a genetically modified plant having improved **stress** tolerance as a result of increasing levels of homoserine acetyltransferase (HAT). The present invention further provides constructs and methods for generating the **stress** tolerant plant. Genes for homoserine acetyltransferase and acetylhomoserine sulfhydrylase of Saccharomyces cerevisiae and Leptospira meyeri were placed under control of vegetative plant or seed-specific promoters and introduced into tobacco by Agrobacterium-mediated

transformation. T3 **transgenic** plants expressing the Saccharomyces cerevisiae MET2 gene for HAT from the cauliflower mosaic virus 35S promoter were normal in appearance. The did not show increased levels of O-acetyl homoserine but did show increased levels of ornithine and arginine. These plants also showed increased resistance to tobacco mosaic virus, paraquat, UV B, and drought, salt and cold **stress**.

L5 ANSWER 45 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 5
AB Transposition of the tobacco retrotransposon Ttol is regulated mainly by transcription from the long terminal repeat (LTR). Functional anal. of the LTR showed that the 13-bp motif is a cis-regulatory element involved in activation by tissue culture, wounding, and treatment with elicitors. The 13-bp motif contains a conserved motif (L box) that has been implicated in the expression of phenylpropanoid synthetic genes in response to defense-related **stresses**. To gain further insight into the regulatory mechanism of the retrotransposon and defense-related genes, cDNAs encoding four different proteins binding to the 13-bp motif were isolated and characterized. One protein is identical to the previously reported NtMYB1, the RNA for which is induced by virus infection; the others are also **MYB**-related factors. One of these factors, NtMYB2, was analyzed in detail. NtMYB2 mRNA was induced by wounding and by treatment with elicitors. NtMYB2 activated expression from the promoter with the 13-bp motif and from the promoter of the phenylalanine ammonia lyase gene (Pv-PAL2) in tobacco protoplasts. Overexpression of NtMYB2 cDNA in **transgenic** tobacco plants induced expression of Ttol and a PAL gene. Together, these results indicate that NtMYB2 is involved in the **stress** response of the retrotransposon and defense-related genes.

L5 ANSWER 46 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB A gene coding for a polypeptide of the 11-12 transmembrane domain transporter family having a Mg2+/H+ or Zn2+/H+ exchange activity, herein designated MHX was cloned from Arabidopsis thaliana cv. C-24. An expression vector was constructed from the cloned cDNA with CaMV35S promoter, omega sequence, and nopaline synthase (nos) polyadenylation and termination signal. **Transgenic** tobacco plants **transformed** with the expression vector for MHX are shown to have a lower sodium content as compared with corresponding wild-type plants or a higher dry matter weight upon growth in calcium-rich media as compared with corresponding wild-type plants. These **transgenic** plants are more tolerant to **stress** conditions, particularly high salinity and calcium-rich media, e.g. saline and calcareous soils.

L5 ANSWER 47 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The characterization of a full length cytochrome P 450 (cyt P 450) cDNA clone from Arabidopsis thaliana (CYP83A1) which showed a 2-4-fold transcriptional induction in the shoot apex following a prolonged low temperature treatment is reported. CYP83A1 appears to be encoded by a single copy gene. The gene contains one intron in a position identical to that found in other class A P 450 genes. Putative cis-acting elements implicated in the regulation of phenyl-propanoid/flavonoid biosynthetic genes (SBF-1, **MYB** Ph3, and P-**MYB**) were identified in the promoter region. The coding region was functional in yeast in binding carbon monoxide and tetcyclacis, suggesting that CYP83A1 was produced in its native state enabling it to interact properly with these two cyt P 450 inhibitors. However, no activity could be detected when assayed in P 450-dependent reactions of gibberellin or phenylpropanoid biosynthesis. **Transgenic** Arabidopsis plants expressing sense and antisense transcripts did not show any abnormalities or altered flowering time with or without vernalization.

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(2006) on STN DUPLICATE 6

AB Cauliflower mosaic virus (CaMV) gene VI protein (P6) is an important determinant of symptom expression. Differential display polymerase chain reaction (PCR) was used to identify changes in gene expression in Arabidopsis elicited by a P6 transgene that causes a symptomatic phenotype. We used slot blot hybridization to measure the abundance of mRNAs complementary to 66 candidate PCR products in **transgenic**, CaMV-infected, and uninfected Arabidopsis plants. CaMV-infected and P6 **transgenic** plants showed broadly similar changes in abundance of mRNA species. In P6 **transgenic** plants we detected 18 PCR products that showed unambiguous changes in abundance plus another 15 that showed more limited changes (approximately twofold). CaMV-infected plants showed 17 unambiguous and 13 limited changes. Down-regulated species include those encoding a novel, phenol-like sulfotransferase, and a glycine-rich, RNA-binding protein. Up-regulated species included ones encoding an **myb** protein, glycine-rich and **stress** -inducible proteins, and a member of a previously unreported gene family. CaMV infection causes alterations in expression of many Arabidopsis genes. Transgene-mediated expression of P6 mimics virus infection in its effect on host gene expression, providing a potential mechanism for this process.

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AB The Arabidopsis thaliana mutants fus3, lec1 and abi3 have pleiotropic defects during late embryogenesis. Mutant embryos fail to enter the maturation programme and initiate a vegetative germination pathway instead. Screening for genes which are differentially expressed in the fus3 mutant of Arabidopsis resulted in the isolation of several members of the **MYB** family. **MYB** domain proteins in plants represent an extended gene family of transcription factors, suggesting their participation in a variety of plant specific cellular functions. Here, the authors describe one of these genes, designated AtMYB13, representing a novel member of the **MYB** gene family. The structure of the gene as well as its genomic organisation and localisation are reported. The expression of the gene is regulated by dehydration, exogenous abscisic acid, light and wounding. A chimeric AtMYB13 promoter/GUS gene is tissue-specifically expressed in **transgenic** Arabidopsis plants. The GUS staining was predominantly detected in the shoot apex zone and at the basis of developing flowers. In addition, the AtMYB13 gene promoter is active at branching points of the inflorescence. Furthermore, ectopic expression of the AtMYB13 gene has a characteristic impact on the architecture of the inflorescence leading to peculiar hook structures at pedicel branching points. In addition, some **transgenic** plants exhibit a reversed order of first flowers and axillary buds. These data suggest a function of the AtMYB13 gene product in linking shoot morphogenic activity with environmental as well as intrinsic signals.

L5 ANSWER 50 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN

AB A complementation approach of the yeast fet3fet4 mutant strain, defective in both low- and high-affinity iron transport, was initiated as an attempt to characterize the Fe(III)-mugineic acid (MA) transporter from grasses. A maize cDNA encoding a novel MYC transcription factor, named 7E, was cloned by screening an iron-deficient maize root cDNA expression library on a min. media containing Fe(III)-deoxyMA as a unique iron source. 7E expression restored growth specifically to the fet3 fet4 mutant strain. It did not affect growth rate of a trk1trk2 potassium transport defective yeast strain or parental W303 strain growth rate. No 55Fe uptake increase was observed in 7E **transformed** fet3 fet4 yeast during short-term kinetics. However, the iron accumulation in these cells was 1.3-fold higher than in untransformed cells after a 24-h period. The 7E protein contained 694 amino acids and had a predicted mol. mass of 74.2 kDa. It

had 44% identity with the RAP-1 protein, a 67.9-kDa MYC-like protein from Arabidopsis thaliana which binds the G-box sequence via a basic region helix-loop-helix (bHLH), without requiring heterodimerization with **MYB** proteins. Phylogenic comparisons revealed that the maize 7E protein was related to the Arabidopsis thaliana RAP-1 protein and to the Phaseolus vulgaris PG1. This similarity was particularly evident for the bHLH domain, which was 95% identical between maize 7E and Arabidopsis thaliana RAP-1. 7E, RAP-1 and PG-1 proteins revealed a plant MYC-like sub-family that was more related to the maize repressor-like IN1 than to maize R proteins. 7E mRNA was detected in both roots and leaves by the Northern anal. The amount of 7E mRNA increased, in response to iron starvation, by 20 and 40% in roots and leaves, resp. The relationship between iron metabolism and myc expression in animal cells is discussed.

L5 ANSWER 51 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB A review, with 51 refs. Recent advances in the understanding of mol. pathophysiol. of hepatic fibrosis, especially (1) the mechanism of activation of
Ito cells, (2) the anal. of promoter regions of extracellular matrix biosynthesis, and (3) the role of matrix metalloproteinases (MMPs) and their specific inhibitors (TIMPs, tissue inhibitors of MMPs) in the formation of and the recovery from liver fibrosis were reviewed. It has been known that Ito cells are activated via the expression of c-**myb** and NFκB which is induced by oxidative **stress**, and inhibited by antioxidant (L-α-tocopherol) and butylated hydroxytoluene. The activation mechanism is now being revealed. TGF-β stimulates the human COL1A2 (α2 chain of type I collagen) gene transcription by increasing the affinity of an SP1-containing transcriptional complex bound to an upstream sequence termed the TGF-β-responsive element. Inagaki et al. obtained two passage-possible clones of CFSC-2G, and CFSC-5H from primary cultures of rat Ito cells in fibrotic livers, and developed a **transgenic** mouse which made it possible to monitor the promoter activity of COL1A2 gene in the process of hepatic fibrogenesis. It has been also clarified that activated Ito cells can produce matrix components as well as MMPs. Very recently the authors observed the participation of MMP-1 (matrix metalloproteinase-1) in the recovery from exptl. hepatic fibrosis using RT-PCR and in situ hybridization. MMPs should be investigated in order to clarify the mechanism of matrix degradation seen in the recovery from liver fibrosis exptl. and clin.

L5 ANSWER 52 OF 59 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN DUPLICATE 8
AB In Arabidopsis, the induction of a dehydration-responsive gene, rd22, is mediated by abscisic acid (ABA) and requires protein biosynthesis for ABA-dependent gene expression. Previous experiments established that a 67-bp DNA fragment of the rd22 promoter is sufficient for dehydration- and ABA-induced gene expression and that this DNA fragment contains two closely located putative recognition sites for the basic helix-loop-helix protein MYC and one putative recognition site for **MYB**. We have carefully analyzed the 67-bp region of the rd22 promoter in **transgenic** tobacco plants and found that both the first MYC site and the **MYB** recognition site function as cis-acting elements in the dehydration-induced expression of the rd22 gene. A cDNA encoding a MYC-related DNA binding protein was isolated by DNA-ligand binding screening, using the 67-bp region as a probe, and designated rd22BP1. The rd22BP1 cDNA encodes a 68-kD protein that has a typical DNA binding domain of a basic region helix-loop-helix leucine zipper motif in MYC-related transcription factors. The rd22BP1 protein binds specifically to the first MYC recognition site in the 67-bp fragment. RNA gel blot analysis revealed that transcription of the rd22BP1 gene is induced by dehydration **stress** and ABA treatment, and its induction precedes that of rd22.

We have reported a drought- and ABA-inducible gene that encodes the **MYB**-related protein ATMYB2. In a transient transactivation experiment using Arabidopsis leaf protoplasts, we demonstrated that both the rd22BP1 and ATMYB2 proteins activate transcription of the rd22 promoter fused to the beta-glucuronidase reporter gene. These results indicate that both the rd22BP1 (MYC) and ATMYB2(**MYB**) proteins function as transcriptional activators in the dehydration- and ABA-inducible expression of the rd22 gene.

L5 ANSWER 53 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB A review with 93 refs. Protooncogene- and tumor-suppressor gene proteins serve essential functions in the regulation of proliferation and differentiation of cells. Abnormal regulation or mutation of these genes, or **transformation** with retroviral homologs, may lead to tumor development in animals. In contrast to vertebrates, only a few data on these genes exist in plants and fungi. Plant nuclear protooncogene homologs, such as **myb** and myc, have multiple regulatory functions in metabolic pathways not existing in mammalian cells; they are involved in the complex regulation of anthocyanin (purple pigment) and phlobaphene (red pigment) biosynthesis, lignin production, trichome differentation, dehydration **stress** gene expression and seed development. Apart from these well-characterized roles in plant-specific pathways, few exptl. data have been reported on a functional significance in growth and development. A screening for nuclear protooncogene- and tumor-suppressor gene-related proteins in the myxomycete Physarum polycephalum revealed the existence of homologs of vertebrate c-myc, c-fos, c-jun, p53, and retinoblastoma proteins during the synchronous cell cycle or sclerotization. The p53 homologs of Physarum and Zea mays were shown to be specific for quiescent stages of their life cycles. Plants and lower eukaryotes, such as fungi, may be useful exptl. systems to elucidate novel functions of protooncogene- and tumor-suppressor proteins in cell cycle regulation and development, or to reveal target genes that might be difficult to identify in complex mammalian systems. Recent data indicate that oncogenes and tumor suppressors in animals have more cellular targets than originally proposed; some of these might be as unexpected as in plant secondary metabolism

L5 ANSWER 54 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 9
AB Excessive production of collagen type I is a major contributor to hepatic fibrosis. Activated (myofibroblastic), but not quiescent, hepatic stellate cells (lipocytes) have a high level of collagen type I and α-smooth muscle actin expression. Therefore, stellate cell activation is a critical step in hepatic fibrosis. Here the authors show that quiescent stellate cells were activated by the generation of free radicals with ascorbate/FeSO4 and by malondialdehyde, a product of lipid peroxidn. In addition, stellate cell activation by collagen type I matrix and TGFα was blocked by antioxidants, such as d-α-tocopherol and butylated hydroxytoluene. Moreover, oxidative **stress**, TGFα and collagen type I markedly stimulated stellate cell entry into S-phase, NF-κB activity and c- **myb** expression, which were prevented by antioxidants. C-**myb** antisense oligonucleotide blocked the activation and proliferation of stellate cells induced by TGFα. Nuclear exts. from activated, but not from quiescent, stellate cells formed a complex with the critical promoter E box of the α-smooth muscle actin gene, which was disrupted by c- **myb** and NF-κB65 antibodies, and competed by c- **myb** and NF-κB cognate DNA. C- **Myb** expression was also stimulated in activated stellate cells in carbon tetrachloride-induced hepatic injury and fibrogenesis. This study indicates that oxidative **stress** plays an essential role, through the induction of c-**myb** and NF-κB, on stellate cell activation.

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AB Genes encoding phenylalanine ammonia-lyase (PAL) are expressed in a complex pattern during plant development and in response to light, pathogen ingress, mechanical damage and other **stresses**. Analysis of the promoter of the bean PAL2 gene in **transgenic** tobacco has shown that some regions responsible for developmental expression are functionally compensatory. The minimum sequence containing all cis sequences necessary for developmental patterns of expression is within -254 bp of the transcription start site. Footprinting and electrophoretic mobility shift assay studies of this region revealed potential cis sequences which coincided with the functional domains defined by small deletions and promoter fusions. Mutations in these potential cis sequences in the context of the minimal -254 bp promoter altered tissue-specific expression patterns, confirming the importance of these sequences for expression in vivo. A functional model for the promoter is presented which predicts that three AC-elements, which are possible **Myb** protein binding sites, together with a G-box, interact to direct the complex patterns of tissue-specific expression observed.

L5 ANSWER 56 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN

AB In Arabidopsis thaliana, the induction of a dehydration-responsive gene, rd22, is mediated by abscisic acid (ABA) but the gene does not include any sequence corresponding to the consensus ABA-responsive element (ABRE), RYACGTGGYR, in its promoter region. The cis-regulatory region of the rd22 promoter was identified by monitoring the expression of β-glucuronidase (GUS) activity in leaves of **transgenic** tobacco plants **transformed** with chimeric gene fusions constructed between 5'-deleted promoters of rd22 and the coding region of the GUS reporter gene. A 67-bp nucleotide fragment corresponding to positions - 207 to -141 of the rd22 promoter conferred responsiveness to dehydration and ABA on a non-responsive promoter. The 67-bp fragment contains the sequences of the recognition sites for some transcription factors, such as MYC, **MYB**, and GT-1. The fact that accumulation of rd22 mRNA requires protein synthesis raises the possibility that the expression of rd22 might be regulated by one of these trans-acting protein factors whose de novo synthesis is induced by dehydration or ABA. Although the structure of the RD22 protein is very similar to that of a non-storage seed protein, USP, of Vicia faba, the expression of the GUS gene driven by the rd22 promoter in non-stressed **transgenic** Arabidopsis plants was found mainly in flowers and bolted stems rather than in seeds.

L5 ANSWER 57 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 11

AB Plants respond to drought with physiol. and developmental changes. Many plant genes have been shown to be induced by drought **stress** and function in drought tolerance. We isolated nine independent genes that are responsive to drought in Arabidopsis thaliana and analyzed the structure of their gene products. Sequence analyses of these genes indicate that their gene products may function in protecting cells from dehydration. We also analyzed the expression of these genes under various **stress** conditions. Some of the drought-responsive genes are induced by plant hormone abscisic acid (ABA), but others are not. There seem to be at least three independent signal transduction pathways between initial drought **stress** signal and gene expression. Two of the pathways are ABA-dependent, but one is ABA-independent. Protein synthesis is necessary for one of the ABA-dependent pathways. We precisely analyzed the promoter of two drought-inducible Arabidopsis genes, rd29A and rd29B, in **transgenic** plants, and identified a novel cis-acting element containing 9 bp, TACCGACAT (DRE, Dehydration Responsive Element), that is involved in the ABA-independent response of rd29A to conditions of dehydration or high salt. DRE is also involved in the induction by low temperature, but does not function in the ABA-responsive, slow expression of rd29A. One of **myb**-related genes, Atmyb2, that is responsive to

water **stress** and abscisic acid (ABA) has been cloned from Arabidopsis. Atmyb2 encodes a transcription factor and binds to conserved **MYB** recognition sequence. These results suggest that the ABA-mediated induction of drought-inducible genes whose expression requires protein synthesis may be regulated by the ATMYB2 protein.

L5 ANSWER 58 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
AB The authors have shown previously that c-**myb** expressed in the yeast Saccharomyces cerevisiae mediated efficient transcriptional activation of reporter genes designed with specific **Myb** Recognition Elements (MRE's), confirming that this protooncogene is able to function as a regulator of transcription in that heterologous context. Here the authors show that in yeast, as in higher eukaryotic cells, the central domain of c-**Myb** displays transactivating capacity. In yeast, however the carboxy-terminal region, defined as a neg. regulatory domain in higher cells, activates transcription as well and appears to be a more potent transactivating domain than the central domain itself. Within this region two domains, namely C1 and C2, have been defined that contribute about equally to the activity of the carboxy-terminal region. C1 spans the sequences missing in AMV v-**myb** while C2, which contains the leucine-zipper motif is specifically absent in the E26 v-**myb** in addition to C1. The c-**Myb** DNA-binding domain itself has no effect on the level of transcription in yeast. The authors also show that AMV v-**Myb** stimulates gene expression in yeast with about half the efficiency of full length c-**Myb**. The fact that the carboxy-terminal region either stimulates or inhibits transactivation properties of c-**Myb**, depending on the cellular context, **stresses** the participation of putative c-**Myb** partner protein in **Myb** regulated processes and reopens the question of whether the oncogenic activation of c-**myb** is indeed due to the increased transactivation capacity of its onco derivs.

L5 ANSWER 59 OF 59 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN DUPLICATE 12
AB An Arabidopsis cDNA (Atmyb2) that contains a sequence that encodes a transcription factor, which is a homolog of **MYB**, was cloned from a cDNA library prepared from dehydrated Arabidopsis rosette plants. A gene (Atmyb2) corresponding to the Atmyb2 cDNA was also cloned and its nucleotide sequence was determined. RNA gel blot analysis showed that the Atmyb2 mRNA was induced by dehydration and disappeared upon rehydration. The Atmyb2 mRNA also accumulated upon salt **stress** and with the onset of treatment with abscisic acid. A beta-glucuronidase reporter gene driven by the Atmyb2 promoter was induced by dehydration and salt **stress** in **transgenic** Arabidopsis plants. These observations indicate that Atmyb2 is responsive to dehydration at the transcriptional level. The putative protein (ATMYB2) encoded by Atmyb2 has 274 amino acids, a molecular mass of 32 kD, and a putative DNA binding domain that shows considerable homology to plant **MYB** -related proteins, such as maize C1. A fusion protein that included ATMYB2 was expressed in Escherichia coli, and it bound specifically to oligonucleotides that contained a consensus **MYB** recognition sequence (TAACTG), such as is found in the simian virus 40 enhancer and the maize bronze-1 promoter. Binding was sequence specific, as indicated by a gel mobility shift experiment. These results suggest that a **MYB**-related transcription factor is involved in the regulation of genes that are responsive to water **stress** in Arabidopsis.